

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):



1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.



2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).



3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).



4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."



5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).



6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).



7. SEE ATTACHED VALIDATION REPORT

Other:

INCLUDES
CONTACT
INFO.

Applicant must provide:



An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"



An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification



A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Phillip Gambel
PHILLIP GAMBEL, PH.D
PRIMARY EXAMINER

Please return a copy of this notice with your response.

3/10/09

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=25; hr=18; min=3; sec=53; ms=549;]

=====

Reviewer Comments:

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.

Nadler, Lee M.

Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH
INCREASED IMMUNOGENICITY AND USES THEREFOR

The above (ii) TITLE OF INVENTION: line exceeds the Sequence Rules' required 72-character limit (this includes white spaces). Please insert a hard return after "WITH" above.

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Per the Sequence Rules, the "INFORMATION FOR SEQ ID NO:" heading is always preceded by a "(2)," regardless of the Sequence ID number.

Please do not number this heading consecutively. Replace the above (3) INFORMATION FOR SEQ ID NO:2: with (2) INFORMATION FOR SEQ ID NO:2:. Please do the same with the subsequent sequences.

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTAGAGCACA

Please replace the (10) INFORMATION FOR SEQ ID NO:9: with (2) INFORMATION FOR SEQ ID NO:9:. Please insert a space after each group of 10 nucleotides, and insert the cumulative nucleotide total at the right margin. These errors occur in subsequent sequences, too.

Validated By CRFValidator v 1.0.3

Application No: 10767561

Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-17 17:06:18.746
Finished: 2008-01-17 17:06:19.572
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 826 ms
Total Warnings: 0
Total Errors: 66
No. of SeqIDs Defined: 17
Actual SeqID Count: 1

Error code	Error Description
E 200	Mandatory field label missing: in 2_i_C
E 200	Mandatory field label missing: in 2_ii
E 200	Mandatory field label missing: in 2_vi_D
E 200	Mandatory field label missing: in 2_i_C
E 104	Command to process tag does not exist: Tag: 11
E 104	Command to process tag does not exist: Tag: 11_i
E 104	Command to process tag does not exist: Tag: 11_i_A
E 104	Command to process tag does not exist: Tag: 11_i_B
E 104	Command to process tag does not exist: Tag: 11_i_C
E 104	Command to process tag does not exist: Tag: 11_i_D
E 104	Command to process tag does not exist: Tag: 11_ii
E 104	Command to process tag does not exist: Tag: 11_xi
E 104	Command to process tag does not exist: Tag: 12
E 104	Command to process tag does not exist: Tag: 12_i
E 104	Command to process tag does not exist: Tag: 12_i_A
E 104	Command to process tag does not exist: Tag: 12_i_B
E 104	Command to process tag does not exist: Tag: 12_i_C
E 104	Command to process tag does not exist: Tag: 12_i_D
E 104	Command to process tag does not exist: Tag: 12_ii
E 104	Command to process tag does not exist: Tag: 12_xi

Input Set:

Output Set:

Started: 2008-01-17 17:06:18.746
Finished: 2008-01-17 17:06:19.572
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 826 ms
Total Warnings: 0
Total Errors: 66
No. of SeqIDs Defined: 17
Actual SeqID Count: 1

Error code	Error Description
E 104	Command to process tag does not exist: Tag: 12_i
E 104	Command to process tag does not exist: Tag: 12_i_A
E 104	Command to process tag does not exist: Tag: 12_i_B
E 104	Command to process tag does not exist: Tag: 12_i_C This error has occurred more than 20 times, will not be displayed
E 252	Calc# of Seq. differs from actual; 17 seqIds defined; count=1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH INCREASED IMMUNOGENICITY AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley Hoag
(B) STREET: 155 Seaport Boulevard
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10767561
(B) FILING DATE: 2004-01-28

(vii) PRIOR APPLICATION DATA:

(B) FILING DATE: 28-JAN-2004
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/101,624;
(B) FILING DATE: 26-JUL-1993;
(A) APPLICATION NUMBER: 08/109,393;
(b) FILING DATE: 19-AUG-1993

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Russell, Hathaway P.
(B) REGISTRATION NUMBER: 46,488
(C) REFERENCE/DOCKET NUMBER: WYS-018.04

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACAGGGTGA AAGCTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60		
GAGTGGGGTC ATTTCCAGAT ATTAGGTACAC AGCAGAAGCA GCCAAA ATG GAT CCC	115		
Met Asp Pro			
1			
CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163		
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu			
5	10	15	
CTC TCT GGT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211		
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr			
20	25	30	35
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259		
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser			
40	45	50	
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307		
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu			
55	60	65	
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355		
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met			
70	75	80	
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403		
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn			
85	90	95	
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451		
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys			
100	105	110	115
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499		
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser			
120	125	130	

GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	135	140	145	
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	150	155	160	595
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	165	170	175	643
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	180	185	190	691
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	200	205	210	739
AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	215	220	225	787
TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	230	235	240	835
GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	245	250	255	883
GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	260	265	270	931
CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	280	285	290	979
AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	295	300	305	1027
GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp	310	315	320	1075
AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCCA AAAAAAAA Lys Ser Asp Thr Cys Phe	325			1120

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
1 5 10 15

Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
50 55 60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65 70 75 80

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
85 90 95

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
100 105 110

His His Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
115 120 125

Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
130 135 140

Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145 150 155 160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
165 170 175

Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
180 185 190

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
195 200 205

Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210 215 220

Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225 230 235 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245 250 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys

260 265 270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
275 280 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290 295 300

Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

(4) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 1151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 99..1028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60

CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC 104
Met Asp
1

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CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG      152
Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu
          5           10          15

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CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG 200
 Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly
 20 25 30

ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG 248
 Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu
 35 40 45 50

AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC 286
 Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr
 55 60 65

GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC 342
 Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr
 79 80 81 82 83 84 85 86 87 88 89 90

CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC			
Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His			
85	90	95	
AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA			440
Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys			
100	105	110	
AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG			480
Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu			
115	120	125	130
TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT			536
Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn			
135	140	145	
GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT			564
Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly			
150	155	160	
CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT			632
His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn			
165	170	175	
GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG			680
Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu			
180	185	190	
TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG			728
Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp			
195	200	205	210
CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC			776
His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser			
215	220	225	
TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT			814
Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr			
230	235	240	
TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG			872
Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met			
245	250	255	
CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC			920
Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro			
260	265	270	
AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG			968
Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu			
275	280	285	290
ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA			1016
Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro			
295	300	305	

AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT 1068
Asn Ala Glu

TTGCCTGAAA TAAGAACGT GC AGAGTTCTC AGAATTCAA AATGTTCTCA GCTGATTGGA 1115
ATTCTACAGT TGAATAATTA AAGAAC 1151

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr
1 5 10 15

Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe
20 25 30

Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile
35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val
50 55 60

Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala
65 70 75 80

Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg
85 90 95

Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile
100 105 110

Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr
115 120 125

Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
130 135 140

Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
145 150 155 160

Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
165 170 175

Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
180 185 190

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
 195 200 205

 Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
 210 215 220

 Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
 225 230 235 240

 Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu
 245 250 255

 Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
 260 265 270

 Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
 275 280 285

 Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
 290 295 300

 Lys Pro Asn Ala Glu
 305

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACCA TCTCAGAAAGT 60

 GGAGTCTTAC CCTGAAATCA AAGGATTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120

 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTT 180

 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240

 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTT CACTTTGAC 300

CCTAAGCATC TGAAGGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
-30 -25

AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
-20 -15 -10

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
-5 1 5 10

GTG GCA AC